

ABSTRACT OF THE DISCLOSURE

A method of preparing an alignment of a protein with known biological function stored in a database and a polypeptide with unknown biological function which comprises the steps of calculating a homology score based upon the coincidence of each constituent amino acid of a protein of known biological function to a polypeptide of unknown biological function and the importance score for the appearance of a biological function, and preparing an alignment representing homology of sites where said importance score is high.